

ID NME311654 standard; genomic DNA; PRO; 3204 BP.
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 DT 17-MAR-2001 (Rel. 67, Created)
 DT 24-JUL-2002 (Rel. 72, Last updated, Version 2)
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 DE Neisseria meningitidis ausP gene for autotransporter serine protease
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 KW ausP gene; autotransporter serine protease.
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 OS Neisseria meningitidis
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae;
 OC Neisseria.
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 RP 1-3204
 RA Ala'Aldeen D.A.;
 RT ;
 RL Submitted (13-MAR-2001) to the EMBL/GenBank/DDBJ databases.
 RL Ala'Aldeen D.A., Microbiology, University of Nottingham, University
 RL Hospital, Nottingham, NG7 2UH, UNITED KINGDOM.
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 RN [3]
 RX MEDLINE; 22112893.
 RX PUBMED; 12117956.
 RA Turner D., Wooldridge K.G., Ala'Aldeen D.A.A.;
 RT "Autotransported serine protease A of Neisseria meningitidis: an
 RT immunogenic, surface-exposed outer membrane, and secreted protein.";
 RL Infect. Immun. 70(8):4447-4461(2002).
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ID NMIGAPPA standard; genomic DNA; PRO; 1113 BP.
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 DT 11-AUG-1995 (Rel. 44, Last updated, Version 4)
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 KW Igab-domain of IgA protease precursor.
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 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae;
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 RX MEDLINE; 94076337.
 RX PUBMED; 8254661.
 RA Klauser T., Kraemer J., Otzelberger K., Pohlner J., Meyer T.F.;
 RT "Characterization of the Neisseria Iga beta-core. The essential unit for
 RT outer membrane targeting and extra";
 RL J. Mol. Biol. 234(3):579-593(1993).
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 RN [2]
 RP 1-1113
 RA Klauser T.;
 RT ;
 RL Submitted (02-FEB-1993) to the EMBL/GenBank/DDBJ databases.
 RL Thomas Klauser Dr., Infektionsbiologie, Max-Planck-Institut fuer, Biologie,
 RL Spemannstr. 34, Tuebingen, BW, W-7400, Germany
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Nucleotide

Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy

Search for [Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [De](#)Display Show: Send to Get Subse**1: X04835. Neisseria gonorrh...**[gi:44868][Links](#)

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DEFINITION Neisseria gonorrhoeae gene for IgA protease.
ACCESSION X04835
VERSION X04835.1 GI:44868
KEYWORDS IgA protease; inverted repeat; protease; secreted protein; signal peptide.
SOURCE Neisseria gonorrhoeae
ORGANISM Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 4899)
AUTHORS Pohlner, J., Halter, R., Beyreuther, K. and Meyer, T.F.
TITLE Gene structure and extracellular secretion of Neisseria gonorrhoeae IgA protease
JOURNAL Nature 325 (6103), 458-462 (1987)
MEDLINE 87115823
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FEATURES

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Entry information

Entry name	Q06467
Primary accession number	Q06467
Secondary accession numbers	None
Entered in TrEMBL in	Release 01, November 1996
Sequence was last modified in	Release 01, November 1996
Annotations were last modified in	Release 24, June 2003

Name and origin of the protein

Protein name	IgA-specific serine endopeptidase [Fragment]
Synonyms	EC <u>3.4.21.72</u> IgA protease
Gene name	None
From	<u>Neisseria gonorrhoeae</u> [TaxID: <u>485</u>]
Taxonomy	<u>Bacteria</u> ; <u>Proteobacteria</u> ; <u>Betaproteobacteria</u> ; <u>Neisseriales</u> ; <u>Neisseriaceae</u> ; <u>Neisseria</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=R16;
 MEDLINE=94076337; PubMed=8254661; [NCBI, ExPASy, EBI, Israel,
Japan]
Klauser T., Kraemer J., Otzelberger K., Pohlner J., Meyer T.F.;
 "Characterization of the *Neisseria* IgA beta-core. The essential unit for
 outer membrane targeting and extracellular protein secretion."
J. Mol. Biol. 234:579-593(1993).

Comments

FUNCTION: THIS PROTEASE IS SPECIFIC FOR IMMUNOGLOBULIN A.
CATALYTIC ACTIVITY: CLEAVAGE OF IMMUNOGLOBULIN A
 MOLECULES AT CERTAIN PRO-|-XAA BONDS IN THE HINGE REGION.
 NO SMALL MOLECULE SUBSTRATES ARE KNOWN.
MISCELLANEOUS: IGA PROTEASE IS EXCRETED, THE SIGNAL
 PEPTIDE GUIDE THE IGA PRECURSOR TO THE PERIPLASMIC SPACE,
 AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH

THE OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS.

Cross-references

EMBL	Z21615; CAA79739.1; [EMBL / GenBank / DDBJ] - [CoDingSequence] Z21616; CAA79740.1; [EMBL / GenBank / DDBJ] - [CoDingSequence]
PIR	S31831; S31831.
GO	GO:0016021 ; Cellular component: integral to membrane (<i>inferred from electronic annotation</i>). GO:0016787 ; Molecular function: hydrolase activity (<i>inferred from electronic annotation</i>). GO:0004252 ; Molecular function: serine-type endopeptidase activity (<i>inferred from electronic annotation</i>).
InterPro	IPR006315 ; Autotransport. IPR005546 ; Autotransporter. Graphical view of domain structure .
Pfam	PF03797 ; Autotransporter; 1.
TIGRFAMs	TIGR01414 ; autotrans_barl; 1.
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	Q06467 .
PRESAGE	Q06467 .
ModBase	Q06467 .
SWISS-2DPAGE	Get region on 2D PAGE .

Keywords

[Hydrolase](#); [Serine protease](#); [Zymogen](#); [Transmembrane](#).

Features



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Sequence information

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of the partial
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Molecular weight:
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ScanProsite, MotifScan



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 AC Z21615;
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 SV Z21615.1
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 DT 09-FEB-1993 (Rel. 34, Created)
 DT 11-AUG-1995 (Rel. 44, Last updated, Version 6)
 XX
 DE N.gonorrhoeae Igab-domain of IgA protease precursor.
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 KW Igab-domain of IgA protease precursor.
 XX
 OS Neisseria gonorrhoeae
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae;
 OC Neisseria.
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 RL Thomas Klauser Dr., Infektionsbiologie, Max-Planck-Institut fuer, Biologie,
 RL Spemannstr. 34, Tuebingen, BW, W-7400, Germany
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 RA Klauser T., Kraemer J., Otzelberger K., Pohlner J., Meyer T.F.;
 RT "Characterization of the Neisseria Iga beta-core. The essential unit for
 RT outer membrane targeting and extra";
 RL J. Mol. Biol. 234(3):579-593(1993).
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 DR GOA; Q06467.
 DR SPTREMBL; Q06467; Q06467.
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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	VACCINE, vol. 12, no. 6, May 1994, pages 492-498, XP000651455 RUPPERT, A. ET AL.: "OmpA-FMDV VP1 fusion proteins: production, cell surface exposure and immune responses to the major antigenic domain of foot-and-mouth disease virus"	21,36,37
Y	see the whole document	1,2,9, 10,15, 16,38

X	EMBO J., vol. 11, no. 6, 1992, pages 2327-2335, XP002028468 KLAUSER, T. ET AL.: "Selective extracellular release of cholera toxin B subunit by Escherichia coli: dissection of Neisseria IgaA-mediated outer membrane transport"	21,36,37
	see the whole document	

Y	MOLECULAR MICROBIOLOGY, vol. 18, no. 2, 1995, pages 377-382, XP000651438 JOSE, J. ET AL.: "MicroCorrespondence: Common structural features of IgA1 protease-like outer membrane protein autotransporters"	1-3, 5-10, 20-23, 38-40
	see page 378 - page 380	

Y	WO 93 10214 A (GEORGIU, G.) 27 May 1993 see page 6, line 6 - page 10, line 28 see page 12, line 4 - page 13, line 29	1-25

Y	BIO-TECHNOLOGY, vol. 14, no. 2, February 1996, pages 203-208, XP002028469 CORNELIS, P. ET AL.: "Development of new cloning vectors for the production of immunogenic outer membrane fusion proteins in Escherichia coli"	1,2,9-11
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Y	MOLECULAR MICROBIOLOGY, vol. 17, no. 1, 1995, pages 123-135, XP000651454 BENJELLOUN-TOUIMI, Z. ET AL.: "SepA, the major extracellular protein of Shigella flexneri: autonomous secretion and involvement in tissue invasion"	2,4
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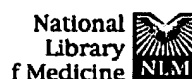
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4:325(6103):458-62.

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Gene structure and extracellular secretion of *N. gonorrhoeae* IgA protease.

Pohlner J, Halter R, Beyreuther K, Meyer TF.

Several human bacterial pathogens, including the Gram-negative diplococcus *Neisseria gonorrhoeae*, produce extracellular proteases that are specific for human immunoglobulin IgA1. Immune (IgA) proteases have been studied extensively and the genes of some species cloned in *Escherichia coli*, but their role in pathogenesis remains unclear. Recently we derived a DNA fragment of 5 kilobases (kb) from *N. gonorrhoeae* MS11 directing expression of an extracellular active enzyme in *E. coli*. Although the mature protease of strain MS11 was shown to have a relative molecular mass of 106,000 (M_r 106K) in gels, the DNA sequence of this cloned fragment reveals a single gene coding for a 169K precursor protease. The precursor contains three functional domains: an amino-terminal leader which is assumed to initiate the intracellular membrane transport of the precursor, the protease, and a carboxyl-terminal 'helper' domain apparently required for extracellular secretion (excretion). Based on the structural features of the precursor, we propose a model in which the protease serves as a pore for excretion of the protease domain through the outer membrane. The protease acquires an active conformation

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outer membrane. IgA protease acquires an active conformation, its extracellular transport proceeds and is released as a monomer from the membrane-bound helper by autoproteolysis. The proform further matures into the 106 K IgA protease and a stable alpha-protein.

PMID: 3027577 [PubMed - indexed for MEDLINE]

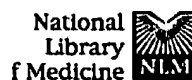
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The great escape: structure and function of the autotransporter proteins.

Henderson IR, Navarro-Garcia F, Nataro JP.

Dept of Medicine, University of Maryland School of Med
Baltimore 21201, USA.

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The autotransporters, a family of secreted proteins from Gram-negative bacteria, possess an overall unifying structure comprising three functional domains: the amino-terminal sequence, the secreted mature protein (passenger domain), and the carboxy-terminal (beta-) domain that forms a beta-barrel to allow secretion of the passenger protein. Members of this family have been implicated as important or putative virulence factors for many Gram-negative pathogens.

Publication Types:

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Volume 234, Issue 3, 5 December 1993, Pages 579-593



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Characterization of the *Neisseria* Iga_β-core

The Essential Unit for Outer Membrane Targeting and Extracellular Protein Secretion

Thomas Klauser, Joachim Krämer, Karin Otzelberger, Johannes Pohlner
and Thomas F. Meyer

Max-Planck-Institut für Biologie Abteilung Infektionsbiologie, Spemannstrasse
34 D-72076 Tübingen, Germany


Available online 29 April 2002.

Abstract

Extracellular transport of *Neisseria* IgA proteases
across the bacterial outer membrane is accomplished
by the translocation function contained within the

C-terminal Iga_{β} domain of IgA protease precursor proteins. Recently, we reported that Iga_{β} from *N. gonorrhoeae* MS11 (Val1097 to Phe1505), fused, to a periplasmic passenger protein, facilitated its transport across the outer membrane, leading to surface exposure of the passenger. In the present work we show, by systematic N-terminal truncation of Iga_{β} , that the functional and structural unit, termed Iga_{β} -core, corresponds to the C-terminal approximately 274 amino acid residues (Ser1231 to Phe1505). This minimal region retains all the essential features necessary for the translocation of an N-terminally attached passenger across the outer membrane of *Escherichia coli*, and for its own correct integration into the outer membrane, even in the absence of a passenger protein. The membrane-integrated Iga_{β} -core constitutes a conserved entity found in the C-terminal regions of Iga_{β} domains of different *N. gonorrhoeae*, *N. meningitidis* and *Haemophilus influenzae* strains. In contrast, the surface-exposed N termini of the Iga_{β} domains vary in size and sequence. Based on secondary structure predictions, the key structural feature of the core is a β -barrel (amphipathic, antiparallel transmembrane β -strands, interspersed by hairpin turns and loops) which is common to many integral outer membrane proteins of Gram-negative bacteria. We propose that the core has been conserved in evolution, to provide a selective outer membrane export channel for covalently attached polypeptides.

Author Keywords: IgA protease; protein secretion; Gram-negative; outer membrane protein; β -barrel

**Journal of Molecular Biology**
Volume 234, Issue 3 , 5 December 1993 , Pages 579-593

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